Claims 17-30 are currently active.

Claims 17 and 23 have been amended.

Antecedent Support

Antecedent support (claim 17) for representing the genotypes of multiple individuals in a DNA mixture at a genetic locus using linear equations is found on page 72, lines 11-15.

Claim Rejections - 35 U.S.C. 112

Claims 17-30 were rejected under 35 U.S.C., second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as invention. This indefiniteness centered on the phrase in part (a) of Claim 17 "obtaining DNA profile data that include a mixed DNA sample".

The amended claims recite the more definite "obtaining DNA profile data of a sample that comprises a DNA mixture of two or more individuals".

Applicant respectfully submits that this amendment fully addresses and adequately overcomes examiner's objections, and requests that the Claims 17-30 (as amended) now be allowed.

Claim Rejections - 35 U.S.C. 102

Claims 17-22, 24, 25, 29, and 30 were rejected under 35 U.S.C. section 102 (b) as being anticipated by Perlin et al. Their paper describes a matrix method for genotyping a mixture of stutter DNA molecules of one individual generated by PCR at one STR locus.

Perlin et al's method specifically describes how to genotype *one individual* using a single matrix equation. Examiner notes that the method applies to "a mixture of stutter DNA molecules," but this prior art does not show how to genotype more than one individual from the same DNA sample. The invention's claims 17-22, 24, 25, 29, and 30 (as now amended) refer to genotyping "a plurality of individuals" using equations. The invention's equations can jointly genotype multiple individuals in the same DNA sample, such as found in DNA mixtures, and therefore go beyond the single-source DNA sample analysis methods described by Perlin et al. Therefore, the claims (as amended) for genotyping multiple individuals were not anticipated by Perlin et al.

Applicant respectfully submits that this amendment fully addresses and adequately overcomes examiner's objections, and requests that Claims 17-22, 24, 25, 29, and 30 (as amended) now be allowed.

Claims 17, 18, 20, 22-24, and 26-30 were rejected under 35 U.S.C. section 102 (b) as being anticipated by Gill et al. Their paper describes an optimization method for genotyping a mixture of DNA molecules generated by PCR using linear equations.

Gill et al's method describes genotyping DNA mixtures using linear equations, but does not perform any matrix operations on these equations. Claims 17, 18, 20, 22-24, and 26-30 (as amended) now refer to "deriving a mathematical solution by performing a *matrix operation* on the linear equations". These claimed matrix operations are entirely novel in the art of DNA mixture analysis. Therefore, the claims (as amended) are not anticipated by Gill et al.

Applicant respectfully submits that this amendment fully addresses and adequately overcomes examiner's objections, and requests that Claims 17, 18, 20, 22-24, and 26-30 (as amended) now be allowed.

Claims 17, 18, 20, 22-24, and 26-30 were rejected under 35 U.S.C. section 102 (b) as being anticipated by Evett et al. Their paper describes an optimization method for genotyping a mixture of DNA molecules generated by PCR using linear equations.

Evett et al's method describes genotyping DNA mixtures using linear equations, but does not perform any matrix operations on these equations. Claims 17, 18, 20, 22-24, and 26-30 (as now amended) specifically refer to "deriving a mathematical solution by performing a *matrix operation* on the linear equations". These claimed matrix operations are entirely novel in the art of DNA mixture analysis. Therefore, the claims (as amended) are not anticipated by Evett et al.

Applicant respectfully submits that this amendment fully addresses and adequately overcomes examiner's objections, and requests that Claims 17, 18, 20, 22-24, and 26-30 (as amended) now be allowed.

Double Patenting

Examiner provisionally rejected Claims 17, 18, 20, 22-24, and 26-30 under the judicially created doctrine of obviousness-type double patenting as being unpatentable over Claims 1, 6-8, and 11 of copending Application No. 09/779096 in view of Gill et al or Evett et al.

Gill et al's method describes genotyping DNA mixtures using linear equations, but does not perform any matrix operations on these equations. Claims 17, 18, 20, 22-24, and 26-30 (as amended) now refer to "deriving a mathematical solution by performing a *matrix operation* on the linear equations". These claimed matrix operations are entirely novel in the art of DNA mixture analysis. Therefore, the claims (as amended) are not anticipated by Gill et al.

Evett et al's method describes genotyping DNA mixtures using linear equations, but does not perform any matrix operations on these equations. Claims 17, 18, 20, 22-24, and 26-30 (as now amended) specifically refer to "deriving a mathematical solution by performing a *matrix operation* on the linear equations". These claimed matrix operations are entirely novel in the art of DNA mixture analysis. Therefore, the claims (as amended) are not anticipated by Evett et al.

Neither Gill et al nor Evett et al show any mathematical methods utilizing *matrix operations* on linear equations that perform the method of the copending claims. Therefore, it would not have been obvious to a person of ordinary skill in the art at the time the invention was made to modify the method of Claims 1, 6-8, and 11 of copending Application No. 09/779096 by use of matrix operations on linear equations.

Applicant respectfully submits that this amendment fully addresses and adequately overcomes examiner's objections, and requests that Claims 17, 18, 20, 22-24, and 26-30 (as amended) now be allowed.

The Examiner provisionally rejected Claims 17-22, 24, 25, 29, and 30 under the judicially created doctrine of obviousness-type double patenting as being unpatentable over Claims 1, 6-8, and 11 of copending Application No. 09/779096 in view of Perlin et al.

Perlin et al's method specifically describes how to genotype *one individual* using a single matrix equation. Examiner notes that the method applies to "a mixture of stutter DNA molecules," but this prior art does not show how to genotype more than one individual. The invention's claims 17-22, 24, 25, 29, and 30 (as now amended) refer to genotyping "a plurality of individuals" using equations. The invention's equations can jointly genotype multiple individuals in the same DNA sample, such as found in DNA mixtures, and therefore go beyond the single-source DNA sample analysis methods described by Perlin et al. Therefore, the claims (as amended) for genotyping multiple individuals were not anticipated by Perlin et al.

Perlin et al does *not* show any method for the analysis of mixed DNA sample comprised of *multiple individuals* that perform the method of the copending claims. Therefore, it would not have been obvious to a person of ordinary skill in the art at the time

the invention was made to modify the method of Claims 1, 6-8, and 11 of copending

Application No. 09/779096 by use of the vector matrix linear equation analysis of a mixed

DNA sample comprised of multiple individuals.

Applicant respectfully submits that this amendment fully addresses and

adequately overcomes examiner's objections, and requests that Claims 17-22, 24, 25, 29, and

30 (as amended) now be allowed.

In view of the foregoing amendments and remarks, it is respectfully requested

that the outstanding rejections and objections to this application be reconsidered and

withdrawn, and Claims 17-30, now in this application be allowed.
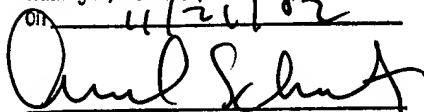
Respectfully submitted,

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17. A method for analyzing a DNA mixture comprised of the steps:

(a) obtaining DNA profile data of a sample that [include a mixed DNA sample] comprises a DNA mixture of two or more individuals;

(b) representing the data and a genotype of the individuals contained in the DNA mixture in a set of linear equations;

(c) deriving a mathematical solution [from] by performing a matrix operation on the linear equations; and

(d) determining the genotype at a locus of an individual contained in the DNA mixture from the mathematical solution.

23. A method as described in Claim 17 wherein the determining step (d) produces an estimate of a proportion or weight of an individual's DNA contained in the [mixed DNA sample] DNA mixture.